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Run on:

Sequence:

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AL449928 Streptoco
AX571762 Sequence
AX454068 Streptoco
AX454068 Streptoco
AX54169 Sequence
CQ645750 Sequence
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COCHIMUATION (8 Of
CONTINUATION (8 OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith, H.E.
Environmentally regulated genes of Streptococcus suis
Patent: WO 02061070-A 39 08-AUG-2002;
ID-Lelystad, Instituut voor Dierhouderij en Diergezondheid B.V.
(NL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTTTGGGGATGGATTGGAGCTGGCCCTCCTGACCACCTATNTGCATCAAGTGCCAAA
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99.0%; Score 260.4; DB 6; Length
Best Local Similarity 99.6%; Pred. No. 7.3e-71;
Matches 262; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACGAAAATDGATGGATCCATGCATAAACTGCATCCCTTAACTTGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .263
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="taxon:32630"
/nole="nucleotide sequence of ivs 31"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            other sequences; artificial sequences
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Sequence 39 from Patent WO02061070.
AX528970
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AE008461
SPREU1906
AX571762
AX57162
AX454067
AX554169
AX554169
AX5645750
AX605546
AX065546
AX065546
AX010037
AE010037
CP000017-07
CP000017-07
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VERSION
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SOURCE
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JOURNAL
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AX528970
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AF333227 Streptoco
AF56303 Streptoco
AF438158 Streptoco
Continuation (9 of
Continuation (9 of
Continuation (9 of
AR120267 Sequence
BD663276 Sequence
AR568696 Sequence
AK568696 Sequence
AK568696 Sequence
AK568696 Sequence
AK568696 Sequence
AR481615 Sequence
                                                                                                                                         ; Search time 2159 Seconds (without alignments) 6924.422 Million cell updates/sec
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Compugen Ltd
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                                                                                                         Bw model
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AR653221
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AR218800
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Gapop 10.0 , Gapext 1.0
                              GenCore (c) 1993
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Maximum Match 100%
Listing first 45 su
                                                                                                         nucleic search, using
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                            Title:
Perfect score:
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Minimum I Maximum I

Database

Searched:

PAT 21-NOV-2002

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Gaps

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120

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Regult No.

셤 ò 셤 ORGANISM

REFERENCE AUTHORS

TITLE

REFERENCE AUTHORS

JOURNAL

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Artables Streptococcus suis fibronectin/fibrinogen binding protein (fbps) gene, complete cds; and alpha-acetolactate decarboxylase gene, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MSFDGFFLHHMTABLRANLEGGRIQKINOPFEQEIVLNIRSNRQ
SHKLLLSAHSVFGRVQLTQSDFTNPRVPNTFTMILRKYLQGAIIERTRQLDNDSILEF
SVSNKODEIGHILQATLIVEIMCKHSNIILVDKSEQKIIEATKHVGFSQNSYRTILPGS
TYIRPPETHSLNPYTVSDEKLFEILSTPQELSPKNLQCOVÇĞLGRDTASELANHLQIDR
LKNFRAFFDQATQPSFLTDKSYAALPFNSPENQPHFBSLSSLLDFYYQDKAEDRKVAQ
QANELIKRVASELEKNRKKLIKQEGGLADTETAELVRQKGELLTTYLHQVPNDQSSVR
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DTMLGQASLAEIDEIREELIETGYLKRRHREKIHKRQKPERYLATDGKTIILVGKNNL
QNDELTFKMAKKGELWFHAKDIPGSHVVITDNLDPSDEVKTDAAELAAYFSKARHSNL
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de Greeff, A., Buys, H., Verhaar, R., Dijkstra, J., van Alphen, L. and
                         of FbpS Gene of Streptococcus suis
                                                                                                                                                      of Veterinary Medicine, Nanjing
Tongwei Road, Nanjing, Jiangsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1034 CTCCTGACCTATCTGCATCAGTGCCAAATGACCAGTCGAGTGTGCGGTTAGACAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 CTCCTGACCACCTAINTGCAICAAGTGCCAAATGACCAGTCGAGTGTGCGGTTAGACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 TACTATACGGGCAAGGAACTGGAGATTGAGTTGGATGTGGCTTTGACTCCTAGCCAAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.2%; Score 174; DB 1; Length 1938; 99.4%; Pred. No. 1.5e-43; Artive 0; Mismatches 1; Indels (
                                                                                    Sun, L., Fan, H. and Lu, C.

Sun, L., Fan, H. and Lu, C.

Direct Submission
Submitted (03-MAR-2004) College of Veterin
Agricultural University, No. 1 Tongwei Roa
210095, P.R. China
Location/Qualifiers
1. 1938
//mol type="genomic DNA"
/strain="9801"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="fbps"
/note="fn/fgn-binding protein"
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/db_xref="G1:45549556"
                                                                                                                                                                                                                                                                                                                                     /serotype="2"
/specific_host="swine"
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/country="China"
Sun, L., Fan, H. and Lu, C.
Cloning and Sequence Analysis
Serotype 2 HA9801 Strain
Unpublished
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Bacteria; Firmicutes;
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Best Local Similarity
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REFERENCE
AUTHORS
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Streptococcus suis clone ivs 31 in vivo selected promoter sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (07-SEP-2000) Department of Bacteriology, Institute for Animal Science and Health, P.O.Box 65, Lelystad 8200 AB, The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Environmentally regulated genes of Streptococcus suis: identification by the use of iron-restricted conditions in vitro
TACTATACGGGCAAGGAACTGGAGATTGAGTTGGATGGGATTGACTTGACTTGACTCCTAGCCAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCCTGACCACCTAINTGCATCAAGTGCCAAATGACCAGTCGAGTGTGCGGTTAGACAAC
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Smith, H.E., Buijs, H., de Vries R, R., Wisselink, H.J.,
Stockhofe-Zurwieden, N. and Smits, M.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and by experimental infection of piglets Microbiology 147 (Pt 2), 271-280 (2001)
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/clone="ivs 31"
                                                                    CAAGGAGGCGGTCAAGCACCTGA 263
                                                                                                          241 CAAGGAGGCGGTCAAGCACCTGA 263
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Best Local Similarity 100.
Matches 175; Conservative
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DEFINITION

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ACCESSION VERSION

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of CP000023 from base 800001 (CP000023 Streptococcus thermophilu
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of CP000024 from base 800001 (CP000024 Streptococcus thermophilu
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OYDDMIERAFANL
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                                                                                                                     de Greeff, A., Buys, H., Verhaar, R., Dijkstra, J., van Alphen, L. and Smith, H.
Smith, H.
Submitssion
Submitted (22-OCT-2001) Infectious Diseases and Food Chain Quality, ID-Lelystad, Edelhertweg 15, Lelystad NL-8219PH, The Netherlands
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              Smith, H.E. Contribution of fibronectin-binding protein to pathogenesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                        /organism="Streptococcus suis"
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/db_xref="taxon:1307"
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/gene="fbps"
                                                         Streptococcus suis serotype 2
Infect. Immun. 70 (3), 1319-1325 (2002)
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db_xref="GI:19110786"
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'rpt_type=inverted
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/gene="fbps"
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/gene="fbps"
235. .241
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/gene="fbps"
/note="FBPS"
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gene="fbps"
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1 (bases 1 to 1423)
Choi,G.H., Kunsch,C.A., Barash,S.C., Dillon,P.J., Dougherty,B., Fannon,M.R. and Rosen,C.A. and Rosen,C.A. streptococcus pneumoniae antigens and vaccines Parent: US 6573082-A 59 03-JUN-2003;
Human Genome Sciences, Inc.; Rockville, MD
Location/Qualifiers
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C12N15/31, C12N5/18, C12N1/21, C07K14/315, C12Q1/68, A61K39/09,
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Pred. No. 1.9e-15;
0; Mismatches 56; Indels
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ilarity 67.8%; Pred. No. 1.9e-15;
Conservative 0; Mismatches 56
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Sequence 59 from patent US 6573082.
AR340958
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Sequence 59 from patent US 6887663.
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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/organism="unknown"
/mol_type="genomic DNA"
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                                                                          Strandedness: Double;
Topology: Linear;
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Best Local Similarity 67.8%;
Matches 118; Conservative 0
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                       G01N33/569,
PC G01N33/68
CC Strandednes
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FH Key
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Matches 118; Conserv
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| Kunsch, C.A., Choi, G.H., Johnson, S.L. and Hromockyj, A.
| Streptococcus pneumoniae antigens and vaccines
| Patent: JP 2001505415-A 30 24-APR-2001;
| Patent: JP 2001505415-A/30
| Patent: JP 200150
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                                                    CTCCTGACCACCTAINTGCATCAAGTGCCAAATGACCAGTCGAGTGTGCGGTTAGACAAC
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     51; Indels
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Choi,G.H., Kunsch,C.A., Barash,S.C., Dillon,P.J. Fannon,M.R. and Rosen,C.A.
Streptcoccus pneumoniae antigens and vaccines Patent: US 6159469-A 59 12-DEC-2000;
Location/Qualifiers
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     0; Mismatches
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/wol_type="unassigned DNA"
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Best Local Similarity 67.8
Matches 118; Conservative
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  Matches 124; Conservative
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                                                                                                                                                                                                                       Houseweart, C.E.

Nucleic acid and amino acid sequences relating to Streptococcus pneumoniae for diagnostics and therapeutics
Patent: US 669703-4 2519 02-WAR-2004;
Genome Therapeutics Corporation; Waltham, MA
Location/Qualifiers
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Doucette-Stamm, L., Bush, D., Zeng, Q., Opperman, T. and
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67.8%; Pred. No. 1.9e-15;
ive 0; Mismatches 56; Indels
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Doucette-Stamm.L.A. and Bush, D.
Nucleic acid and amino acid sequences relating pneumoniae for diagnostics and therapeutics
Patent: 105 6800/74-A 1976 05-00T-2004;
Genome Therapeutics Coxporation; Waltham, MA Location/Qualifiers
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                                                          AR481615 1683 bp DN.
Sequence 2519 from patent US 6699703.
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/mol_type="genomic DNA"
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                                                                                                           Barash, S.C., Dillion, P.J., Dougherty, B.,
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Streptococcus pneumoniae proteins and nucleic acids
Patent: WO 02077021-A 1903 03-OCT-2002;
Chiron Spa (IT); THE INSTITUTE FOR GENOMIC RESEARCH
Location/Qualifiers
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Pred. No. 1.9e-15;
0; Mismatches 56; Indels
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Choi.G.H., Kunsch.C.A., Barash,S.C., Dillion,P. Choi.G.H., Kunsch.C.A., Barash,S.C., Dillion,P. Streptococcus pneumoniae SP036 polynucleotides Patent: US 6897663-A. 59 03-MAY-2005, Human Genome Sciences, Inc.; Rockville, MD Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:1313"
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1 (bases 1 to 2015)

Holmes,A.R., McNab,R., Millsap,K. and Jenkinson,H.F.

The pavA gene of Streptococcus pneumoniae encodes a adhesion and virulence tibronectin-binding protein that is necessary for Pneumococcal cell adhesion and virulence

Upublished

1 (bases 1 to 2015)

Holmes,A.R., McNab,R. and Jenkinson,H.F.

Birect Submission

Submitted (31-AUG-1999) Oral Sciences and Orthodontics, University of Otation, Qualifiers
                                                                                                                                                                                2015 bp DNA linear BCT 02-NOV-1999 Streptococcus pneumoniae adherence and virulence protein A (pavA) gene, complete cds.
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TYIAPPSTESINPFTIKOBKIPBILQTQBLTAKNIQSLFPGGLGRDTANELERILVSEK
SELIRWYENDETROCTIPETS FSPPPRANGAGEPPANISDLIDTYKWYARARDRYKYQA
SELIRWYENDETROCKERILATDNABEFRQKGELLTTFLHOYPDDQDQVILD
NYYTNQPIMIALDKNAHTGAKOBRELLATDNABEFRQKGELLTTFLHOYPDDQDQVILD
NYYTNQPIMIALDKALTPNQNAQRYFKRYQKKKLEQYLTDLIBETKATILYLESVET
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BELIFKWARKEELWFFAKDIFGSHVISGNLDPSDAVKTDAABLAAYFSQGRLSNLVQ
VDMIBVKGLNKFPGGKKGFVTYTGQKTLRVTPDSKKLASMKKS:
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SHRLLLSAHPVFGRIQLTQTTFENPAQPSTFIMVLRKYLLQALIESIEQVENDRIVEI
TVSNKNEIGDHIQATLIIEIMGKHSNILLVDKSSHKILEVIKHVGFSQNSYRTLLPGS
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protein_id="AAF06332.1"
db_xref="GI:6175915"
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/function="adhesin"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4586 ACTATACCAACCAACCTATCATGATTGCGCTTGATAAGGCTCTGACTCCGAACCAAGAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4526 CCCAACGCTATTTTAAACGGTATCAGAAACTCAAAGAAGCTGTCAAATACTTGA 4473
                      1174 CCCAACGCTATTTTAAACGGTATCAGAAACTCAAAGAAGCTGTCAAATACTTGA 1227
210 CCCAGCGGTACTTCAAGAAGTACCAGAAACTCAAGGAGGCGGTCAAGCACCTGA
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2e-15;
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Pred. No. 2e-19
0; Mismatches

    .10240
    /organism="unidentified"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32644"

                                                                                                                                                                     CQ788941 10240 bp
Sequence 32 from Patent EP1400592.
CQ788941. GI:45822509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                   unidentified unclassified sequences.
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Best Local Similarity 67.8%;
Matches 118; Conservative (
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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Listing first 45 summaries
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263
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SUMMARIES

		Description	Abs59824 Streptoco	Aav27353 Streptoco	Abq84821 S. pneumo	Adc45140 S. pneumo	Adm91909 S pneumon	Abx06664 S. pneumo	Aas55569 Streptoco	Aca49876 Prokaryot	Adk46004 Streptoco	Adr93341 Novel, S.	Aea57211 Streptoco	Aav52165 Streptoco	Continuation (8 of	Continuation (9 of	Aca50476 Prokaryot	Abn67397 Streptoco	Aca48071 Prokaryot	Abn67396 Streptoco	Adv84865 Streptoco	
SUMMAKIES		ID	ABS59824	AAV27353	ABQ84821	0 ADC45140	2 ADM91909	0 ABX06664	AAS55569	ACA49876	3 ADK46004	3 ADR93341 .	4 AEA57211	AAV52165	0 ABS56454 07	0 ABS56454 08	ACA50476	ABN67397	ACA48071	ABN67396	3 ADV84865	
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	Ouerv	Match	99.0	32.3	32.3	32.3	32.3	32.3	32.3	32.3	32.3	32.3	32.3	32.3	32.3	32.3	31.6	31.6	29.0	25.4	25.4	
		Score	260.4	85	85	85	85	85	85	85	85	82	85	85	85	85	83.2	83.2	76.2	8.99	66.8	
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Adv87732 Streptoco Continuation (12 o Continuation (13 o Continuation (14 o Continuation (14 o Continuation (14 o Aav37351 Streptoco Aat39284 Mobilisab Aas17996 GalB gene Aad29902 Plasmid p Ab280625 Plasmid p Ad280625 Plasmid p Ad425766 Vitamin B Aad48463 Plasmid p Ad51075 pOThy12 p Aad51075 pOThy12 p Aad51077 pOThy16 p Aad51077 pOThy16 p Aad51077 pOThy11 p	induced gene; iri; vaccine;	icus for the diagnosis of and ions, comprises the modification unis.  Whating Streptococcus virulence the genomic fragment intifiable by hybridisation in fragment of iron-restricted genes given in the specification, fragment has been modified. The ence of Streptococcus suis that
ADV87732 ADV78985 ABV78985 ABV90521_13 ABV90521_13 ADV81204_13 ADV81204_13 ADV81204_13 ADV81204_13 ADV81204 ADV81204 ADS1076 ADS1076 ADS1076 ADS1076 ADS1077 AADS1077 AADS1077 AADS1078	ALIGNMENTS BP. elected seque n-restricted gene; ds	reptococ 11 infect Scoccus s 11sh. of of mod of it, w part ide acid or acid (1vs) genomic
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222 223 223 223 223 224 225 226 226 226 226 227 226 226 227 227 227	T.1 ABS59824 ABS59824; 05-NOV-20 Streptocc in vivo 8 Streptocc in vivo 8 31-JAN-20 02-FEB-20	Smith HB; WPI; 2002 Modulatin vaccinatio of a geno Disclosur The inven by modifyes Streptoco Streptoco induced (and obtail method is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis.
may be used in the diagnosis of and vaccination against streptococcal infections and in the detection of virilence markers of Streptococci. vaccine comprising the clone, nucleic acid, vector, or the host cell, also useful in the prevention and/or treatment of streptococcal infections. ABSS9987-ABSS9832 represent Streptococcus suis in vivo selected (ivs) genes and related PCR primers of the invention
                                                                                                                                                                                                                                                                                                                                                                                GGATGTGGCTTTGACTCCTAGCCCAAATGCCCAGGGGTACTTCAAGAAGTACCAGAAACT
                                                                                                                                                                                                        1 ACGAAAATCGATGGATCCATGCATAAACTGCATCCCTTAACTTGTTTTTCGTGTGCCCTAT
                                                                                                                                                                                                                                                                                                                         TGACCAGTCGAGTGTGCGGTTAGACAACTACTATACGGGCAAGGAACTGGAGATTGAGTT
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pneumoniae, antigen; vaccine; infection; diagnosis; detection; pneumonia; otitis media; meningitis; ss.
                                                                                                                                                            ;
0
                                                                                                                                DB 6; Length 263;
                                                                                                                              Score 260.4; DB 6; Length
Pred. No. 9e-79;
0; Mismatches 1; Indels
                                                                                                                                                                                      1 ACGAAAATDGATGGATCCATGCATAAACTGCATCCCTTAACTTGTT
                                                                                                    Sequence 263 BP; 72 A; 63 C; 61 G; 66 T; 0 U; 1 Other;
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2. 1423
/*tag= a
/product= "SP0039"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Johnson LS,
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                                                                                                                             Query Match 99.0%;
Best Local Similarity 99.6%;
Matches 262; Conservative (
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P-PSDB; AAW55092.
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The present sequence encodes a protein from Streptococcus pneumoniae. The nucleic acid sequence encoding the Streptococcus pneumoniae protein can be useful in vaccines for inducing protective antibodies against Streptococcus pneumoniae, for treatment or prevention of infection e.g. pneumonia, otitis media or meningitis. Probes based on the nucleic acid are used to detect Streptococcus infection (by usual hybridisation or amplification methods), also for isolating Streptococcus genes or their allelic variants. The protein can be used similarly to detect specific antibodies in standard immunoassays, especially for diagnosing or monitoring infections. Antibodies which bind the protein are used to detect corresponding antigens, to purify the protein and for passive immunisation (optionally coupled to a toxin). Vaccines are administered, e.g. by injection, orally or through the skin, typically at 0.01-1000
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                                                                                                                                                                                                                                                                                                                                                                                           Gape
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                                                                                                                                                                                                                                                                      Sequence 1423 BP; 488 A; 324 C; 281 G; 330 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                    Length 1423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S. pneumoniae SP039 nucleotide sequence SEQ ID NO:59.
                                                                                                                                                                                                                                                                                                   32.3%; Score 85; DB 2; 1 67.8%; Pred. No. 3.3e-18; rative 0; Mismatches 56;
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              Claim 1; Page 60-61; 118pp; English.
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Matches 118; Conservative
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KUNSCH C A.
BARASH S C.
DILLON P J.
DOUGHERTY B.
FANNON M R.
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P-PSDB; ABP54586.
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56; Indels

Length 1423;

149

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WPI; 2003-764574/72.
                                                                                                                                                    P-PSDB; ADC45141.
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30-0CT-1997;
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Rosen CA;
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The invention relates to an isolated polynuclectide consisting of a Streptococcus pneumoniae nucleic acid (appearing as ADC45122 and encoding SP028) one of 113 disclosed nucleic acids encoding 113 S. pneumoniae antigens. Also included are making a recombinant vector by inserting the nucleic acid into a vector, an isolated polynucleotide consisting of at least 50 or 100 contiguous nucleotides of the SP028 nucleic acid, and a recombinant host cell comprising the SP028 polynucleotide. The nucleic acids are useful as DNA vaccine against Streptococcus pneumoniae infection (e.g. pneumonia). Nucleic acids derived from the S. pneumoniae antigen nucleic acids are useful as probes for use in diagnostic methods for detecting S. pneumoniae gene expression. The present sequence encodes an S. pneumoniae antigenic protein.
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Pred. No. 3.3e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 32.3%;
Best Local Similarity 67.8%;
Matches 118; Conservative
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                                                                                                                                                                                                                                                                                                          ABQ84792 to ABQ84904 represents nucleic acids which encode the Streptococcus pneumoniae antigens given in ABPS4557 to ABPS4669. The S. pneumoniae antigens diven in ABPS4557 to ABPS4669. The S. preumoniae antigens can also be used in vaccines. The S. pneumoniae antigens can also be used to prevent or attenuate a Streptococcal infection in an animal. The polynucleotides encoding the S. pneumoniae antigens can be used to detect Streptococcus nucleic acids. ABQ84905 to ABQ85130 represent primers used in the cloning of S. pneumoniae ORFs (open reading frames) which are used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTATACGGGCAAGGAACTGGAGATTGAGTTGGATGTGGCTTTTGACTCCTAGCCAAAATG 209
                                   New Streptococcus pneumoniae antigens, useful for detecting Streptococcus and for preventing or attenuating disease caused by Streptococcus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCTGACCACCTAINTGCATCAAGTGCCAAATGACCAGTCGAGTGTGCGGTTAGACAACT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCAACGCTATTTTAAACGGTATCAGAAGTCAAAGAAGCTGTCAAATACTTGA 890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1423 BP; 488 A; 324 C; 281 G; 330 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 85; DB 6; I
Pred. No. 3.3e-18;
0; Mismatches 56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S. pneumoniae DNA encoding antigen SP039,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barash SC,
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                                                                                                                                                                                                                                                     Claim 1; Page 28; 70pp; English
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Best Local Similarity 67.8
Matches 118; Conservative
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This invention relates to novel isolated Streptococcus pneumoniae nucleic acid molecules and the antigenic polypeptides encoded by them. The invention may be useful for the production of compounds with an antibacterial activity or for gene therapy. The nucleic acid molecules, compositions and methods disclosed are useful for treating Streptococcus
                                                                                                                                                                                                                                                                                                                                                    New Streptococcus pneumoniae nucleic acid molecules, useful for diagnosing, treating and preventing active infections of Streptococcus
                                                                                     antibacterial; gene therapy; Streptococcus pneumoniae infection;
                                                           S pneumoniae antigenic protein-encoding gene sequence SeqID106.
                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, SEQ ID NO 106; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                    pneumoniae
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encoding Streptococcus pneumoniae polypeptides vaccines for prevention or attenuation of infection

Novel polynucleotide encoding useful for producing vaccines

by Streptococcus pneumoniae.

Example 1; SEQ ID NO 59; 58pp; English.

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1006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a protein comprising or having at least 50% identify to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS56454. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the sequence not defined in the specification, for amplifying a target sequence contained within a Streptococcus nucleic acid sequence, where
                                                                                                                                                                                 947 İGCTGACAACCTTCCTCCACCACCAAGTGCCTAACGACCAAGACCAGGTTATCCTAGACAACT
                                                                                                                                                           90 TCCTGACCACCTAINTGCATCAAGTGCCAAATGACCAGTCGAGTGTGCGGTTAGACAACT
                                                                                                                                                                                                                                  150 ACTATACGGGCAAGGAACTGGAGATTGAGTTGGATGTGGCTTTGACTCCTAGCCAAAATG
pneumoniae infection. The present sequence is that of an S pneumoniae
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                            1067 CCCAACGCTATTTTAAACGGTATCAGAAACTCAAAGAAGCTGTCAAATACTTGA 1120
                                                                                                                                                                                                                                                                                                       263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene; ds; bacterial meningitis; pneumonia; sepsis; otitis media; ear infection; antiinflammatory; antibacterial; immunostimulant;
                                                                                                                                                                                                                                                                                                       CCCAGCGGTACTTCAAGAAGTACCAGAAACTCAAGGAGGCGGTCAAGCACCTGA
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                                                                                       Length 1653;
                                                  Seguence 1653 BP; 551 A; 383 C; 322 G; 397 T; 0 U; 0 Other;
                                                                                                                         56; Indels
                                                                                    Score 85; DB 12;
Pred. No. 3.6e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pneumoniae type 4 strain coding region #952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                auditory; respiratory; gene therapy, vaccine.
                                                                         32.3%; bcc. No. 5...
67.8%; Pred. No. 5...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fraser C;
                                                                                                                                                                                                                                                                                                                                                                                                                                 ABX06664 standard; DNA; 1680 BP
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                                                                                                                       Matches 118; Conservative
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                gene of the invention.
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                                                                                                      Local Similarity
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11-FEB-2003
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                                                                                      Query Match
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the first primer is substantially complementary to the target sequence
and the second primer is substantially complementary to the complement of
the target sequence, and where the parts of the primers having
substantial complementarity define the termin of the target sequence to
substantial complementarity define the termin of the target sequence to
be amplified, assay comprising contacting a test compound with the
complementarity and the set compound binds to the protein
and a Streptococcus pneumoniae bacterium, where one or more genes
conciding the proteins has been rendered inactive. The proteins, nucleic
acid molecules, antibody and compositions are useful as medicaments for
treating or preventing a disease or infection due to streptococcus
catedia, particularly S. pneumoniae, such as pneumonia, sepsis, otitis
media or ear infection. They are also useful in developing vaccines,
catediagnostics and antibiotics. The methods are useful for identifying
immunodominant proteins. The present sequence is one of the 2489
cidentified coding region from the genomic sequence. Note: The sequence
condens of this patent did not form part of the printed specification, but
was obtained in electronic format directly from WIPO at
cipy wipo.int/pub/published_pcc_sequences. (Updated on 27-OCT-2003 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae DNA for cellular proliferation protein #140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210 CCCAGCGGTACTTCAAGAAGTACCAGAAACTCAAGGAGGCGGTCAAGCACCTGA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense; ds; prokaryotic cellular proliferation gene; antibiotic; antibacterial; drug design.
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                                                                                                                                                                                                                                                                                                                                                                                                           Length 1680;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           DB 10;
3.6e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                         Score 85; DB 1
Pred. No. 3.6e-
0; Mismatches
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2000US-0207727P.
2000US-0242578P.
2000US-0253625P.
2000US-025393P.
                                                                                                                                                                                                                                                                                                                                                                                                           32.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 67.8
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200170955-A2.
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26-MAY-2000; 2
23-OCT-2000; 2
27-NOV-2000; 2
22-DEC-2000; 2
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Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-SEP-2001
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(ELIT-) ELITRA PHARM INC.
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                                                         Wang L,
Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
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                                                                                                                                                                                                                    The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, the prokaryotic cellular proliferation, their use in identifying the genes, the their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Bscherichia coll, Staphylococcus aureus, Salmonalla typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also cuseful for the identification of potential new targets for antibiotic development. The antisense mucleic acids cands be used to identify proteins used in proliferation, to express these proteins, and to obtain antisense mucleic acids to express these proteins. The proteins can takense mucleic acids equence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Mote: The sequence data for this patent of the printed specification, but was obtained in the first control of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90 TCCTGACCACCTATNTGCATCAAGTGCCAAATGACCAGTCGAGTGTGCGGTTAGACAACT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 ACTATACGGGCAAGGAACTGGAGATTGAGTTGGATGTGGCTTTGACTCCTAGCCAAAATG 209
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                                                                                        New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1683 BP; 565 A; 387 C; 331 G; 400 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 1683;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 85; DB 4; Pred. No. 3.6e-18; 0; Mismatches 56
                                                                                                                                                                                Claim 27; SEQ ID NO 9206; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACA49876 standard; DNA; 1683 BP
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2001US-0342923P.
2002US-00072851.
2002US-0362699P.
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Best Local Similarity 67.8%;
Matches 118; Conservative
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         2001-611495/70.
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         WPI; 2001-611495,
P-PSDB; AAU37710
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25-OCT-2001;
08-PEB-2002;
06-MAR-2002;
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The invention relates to an isolated nucleic acid compilating of the following the following a month of a cell. Also included are:

the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibite proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense continuous antisense incleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide of its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding continuous the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, or that has an activity against a biological pathway continuous and activity of a gene in an operon required for proliferation or that has an activity against a biological pathway in which a proliferation, or that inhibits cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound sactivity; (11) a culture comprising strains in which the gene or which each of the strains is present in a culture or collection of the strains in greent in a culture or collection of the strains in greent in a culture or collection of the strains; or (13) identifying the target of a compound that inhibits the continuous of the strains in spresent in a culture or collection of continuous or societing for homologous nucleic acids are useful or required for proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required continuous or presenting for homologous nucleic acids required continuous or presenting for homologous nucleic acids are useful continuous or presenting genes. Note: The sequence is one of the target of prokaryotic essential genes. Note: The sequence at so this patent did continuous or present and present sequenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1093
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                                                                                                                                                                                                                                                                                                                                                                                                                                 invention relates to an isolated nucleic acid comprising any one of
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Zyskind JW;
Xu HH;
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                                                                                                                                                                                                                                                  t
                                                                                                                                                                                                             New antisense nucleic acids, useful for identifying proteins or s
for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
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Pred. No. 3.6e-18;
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   Ohlsen KL,
Forsyth RA,
   Haselbeck R,
Yamamoto R,
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                                                                                                                                                                                                                                                                                                                                                                  Claim 14; SEQ ID NO 37746; 1766pp; English
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       Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADK46004 standard; DNA; 1683
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Best Local Similarity 67.8
Matches 118; Conservative
       Zamudio C,
Trawick JD,
                                                                                                        WPI; 2003-029926/02.
P-PSDB; ABU46006.
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The invention relates to an isolated nucleic acid comprising a sequence encoding a Streptococcus pneumoniae ADR91366polypeptide, or its fragments, with any of 9 fully defined sequences (appearing as ADR9408, ADR94489, ADR94800, ADR94801, ADR94801, ADR95612, ADR956212, ADR956079) or any of the fully defined sequences appearing as ADR91705, ADR99186, ADR99186, ADR99186, ADR99186, ADR99186, ADR99180, ADR99186, ADR99180, ADR99186, ADR99186, ADR99186, ADR99186, ADR99186, ADR99186, ADR99186, ADR99186, ADR99186, ADR99180, CC ADR99186, ADR99180, AD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid encoding a Streptococcus pneumoniae polypeptide, useful for diagnosing, preventing and/or treating pathological conditions resulting from the bacterial infection.
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Pred. No. 3.6e-18;
0; Mismatches 56; Indels
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                                                                                                                                                                                                                                                                                                                                                                                        (GENO-) GENOME THERAPEUTICS CORP.
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98US-0085131P.
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Best Local Similarity 67.8%;
Matches 118; Conservative (
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                                    US6800744-B1
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12-MAY-1998;
                                                                                                             05-0CT-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated Streptococcus pneumoniae nucleic acids and polypoptides. The nucleic acids and proteins are useful for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, such as S. pneumoniae infection. These may also be used for drug screening procedures. The present sequence represents a streptococcus pneumoniae nucleic acid of the invention. Note: The sequence data for this patent did not appear in the printed specification but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149
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                                                                            ds; gene; Antibacterial; Gene therapy; Vaccine; Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid molecules and polypeptides useful for diagnosing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90 TCCTGACCACCTATNTGCATCAAGTGCCAAATGACCAGTCGAGTGTGCGGTTAGACAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preventing and treating pathological conditions resulting from linfection, e.g. Streptococcus pneumoniae infection, and in drug
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Opperman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel S. pneumoniae DNA sequence, SEQ ID 1976.
Streptococcus pneumoniae gene, Seq ID No 2519.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 2519; 301pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENO-) GENOME THERAPEUTICS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        segdata.uspto.gov/seguence.html.
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98US-0085131P.
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                                                                                                                                                         Streptococcus pneumoniae
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30-JUN-1998;
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RESULT 10

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ADR93341

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Streptococcus pneumoniae ORF nucleic acid sequence SEQ ID NO:1976.

New isolated nucleic acid molecules and encoded polypeptides useful for diagnosing, preventing or treating bacterial infections, particularly Streptococcus pneumoniae infection. bacterial infection; Streptococcus pneumoniae infection; antibacterial; Claim 1; SEQ ID NO 1976; 144pp; English 97US-0051553P. 98US-0085131P. 10-JUL-2003; 2003US-00617320 98US-00107433 (DOUC/) DOUCETTE-STAMM L A. (BUSH/) BUSH D. Streptococcus pneumoniae. WPI; 2005-477576/48. Doucette-Stamm LA, vaccine, gene, da. P-PSDB; AEA59814 US2005136404-A1. 02-JUL-1997; 30-JUN-1998; 12-MAY-1998 23-JUN-2005 

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Bush

The invention relates to an isolated nucleic acid molecule for detecting, preventing or treating pathological conditions resulting from bacterial preventing or treating pathological conditions resulting from bacterial concentration. The isolated nucleic acid comprises: (a) any of the 2603 mucleotide sequences of ARA57838; (b) a nucleotide sequence cacid sequences of ARA57838; (c) a nucleotide sequence of ARA57839; (b) a nucleotide sequence of ARA57839; (b) a nucleotide sequence cacid sequences of ARA57839; (c) a nucleotide sequence of ARA57839; (d) a nucleotide sequence of ARA57839; (e) a call comprising the recombinant expression vector comprising the above nucleic acid pathologian expression vector comprising the cabove nucleic acid operably linked to a transcription regulatory element; (d) a call comprising the recombinant expression vector; (3) producing an S. pneumoniae polypeptide; (4) a probe comprising a nucleotide sequence consisting of at least 8 nucleotides of ARA57839; (5) treating a subject for S. pneumoniae infection, (6) a recombinant or substantially pure preparation of an S. pneumoniae polypeptide; (f) a vaccine composition for preventing or treating an S. pneumoniae infection, comprising an amount of the above nucleic acid in a sample; (7) a vaccine composition for preventing or treating an subject (8) detecting the presence of a Streptococcus nucleic acid in a sample; (g) a computer readable medium having recorded the nucleotide sequences of ARA55336 to ARA57839; (10) a computer based system for identifying cramming of the Streptococcus genome of commercial infection and methods are useful for diagnosing, preventing or treating bacterial infections, particularly S. pneumoniae infection. The present composition has a sequence of sequences represents a S. pneumoniae off Parafor Haria naterial for man entited for the paraformant invention where a present dara for this naterial forms. present invention. Note - The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site.

ö TCCTGACCACCTAINTGCATCAAGTGCCAAATGACCAGTCGAGTGTGCGGTTAGACAACT 149 Gaps ö DB 14; Length 1692; Sequence 1692 BP; 567 A; 387 C; 332 G; 406 T; 0 U; 0 Other; 56, Indels Pred. No. 3.6e-18; 0; Mismatches 56 Score 85; 32.3%; Best Local Similarity 67.8%; Matches 118; Conservative 8 Query Match

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150 ACTATACGGGCAAGGAACTGGAGATTGAGTTGGGCTTTGACTCCTAGCCAAAATG

1043 ACTATACCAACCAACCTATCATGATTGCGCTTGATAAGGCTCTGACTCCCAACCAGAATG 1102 1103 CCCAACGCTATTTTAAACGGTATCAGAAACTCAAAGAAGCTGTCAAATACTTGA 1156 CCCAGCGGTACTTCAAGAAGTACCAGAAACTCAAGGAGGCGGTCAAGCACCTGA 210 셤 ሯ 셤

RESULT 12

Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay; computer readable medium; vaccine; pharmaceutical composition; ds. Streptococcus pneumoniae genome fragment SEQ ID NO:32. AAV52165 standard; DNA; 10240 BP. (first entry) 23-OCT-1998 AAV52165; AAV52165, 

97WO-US019588 Streptococcus pneumoniae 30-0CT-1997; WO9818931-A2 07-MAY-1998.

Fannon M; Barash SC, Rosen CA, Dillon PJ, Choi GH, Dougherty BA; Kunsch CA,

96US-0029960P.

31-OCT-1996;

(HUMA-) HUMAN GENOME SCI INC.

WPI; 1998-272225/24.

Computer-readable medium with recorded Streptococcus pneumoniae polymucleotide sequences - useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus pneumoniae.

Claim 1; Page 326-332; 1409pp; Bnglish.

The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID No:1 to 391 (AAV52134 to AAV52524) recorded on it, or a representative fragment or a sequence at least 95% identical to SEQ ID No: 1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid colecule encoding a homologue of any of the fragments of the S.pneumoniae of probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the library which contain sequences that the members of the library with contain sequences that from the members or (b) isolating mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is hybridise to the target sequence and isolating the nucleic acid molecules or commercial importance, or the amplification primers derived from the fragment of the S. pneumoniae genome to prime the amplification and isolating the amplified sequence is commercial importance, or expression modulating fragments of the S. pneumoniae genome. Produces from the present invention can be used in commercial importance, or expression modulating fragments of the S. pneumoniae genome. Produces from the present invention can be used in diagnosis kits and assays, and pharmaceutical compositions and vaccines for S. pneumoniae

Sequence 10240 BP; 2865 A; 1914 C; 2390 G; 3068 T; 0 U; 3 Other;

Gарв ö DB 2; Length 10240; 32.3%; Score 85; DB 2; Length 1024 67.8%; Pred. No. 8.1e-18; ive 0; Mismatches 56; Indels Best Local Similarity 67.8 Matches 118; Conservative Query Match

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90 TCCTGACCACCTAINTGCATCAAGTGCCAAATGACCAGTCGAGTGTGCGGGTTAGACAACT 149

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
of the nucleic acid inhibits proliferation of a cell. Also included are:
                                                                                                                                                                                                                                                                             7423 ACTATACCAACCAACCTATCATGATTGCGCTTGATAAGGCTCTGACTCCCAACCAGAATG
                                                                                                                                                                                                                                                       150 ACTATACGGGCAAGGAACTGGAGATTGAGTTGGATGTGGCTTTTGACTCCTAGCCAAAATG
                                                                                                                                                                                                     90 TCCTGACCACCTATNTGCATCAAGTGCCAAATGACCAGTCGAGTGTGCGGTTAGACAACT
                                                                                                                                                                                                                              7483 TGCTGACAACCTTCCTCCACCAAGTGCCTAACGACCAAGACCAGGTTATCCTAGACATT
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Xu HH;
                                                                                                                                                                                                                                                                                                                               7310
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense nucleic acids, useful for identifying proteins or scre
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                        210 CCCAGCGGTACTTCAAGAAGTACCAGAAACTCAAGGAGGCGGTCAAGCACCTGA 263
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                                                                                                                                                  Length 110000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense; ds; prokaryotic essential gene; cell proliferation;
                                                                                                                                                                            56; Indels
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Forsyth RA,
                                                                                                                                                     Score 85; DB 10;
Pred. No. 2.3e-17;
; Mismatches 56
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Yamamoto R,
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Carr GJ,
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06-SBP-2001; 2001US-00948993.
25-0CT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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Matches 118; Conservative
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Trawick JD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            design; gene
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ABS56454 12
ABS56454 13
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ABS56454 19
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fragments LOCUS ABSS6454 Accession Abs56454
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ACTATACGGGCAAGGAACTGGAGTTGAGTTGGATGTGGCTTTGACTCCTAGCCAAAATG
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cc (1) a vector comprising a promoter operably linked to the mucleic acid cuciding a polypeptide whose expression is inhibited by the antisense conding a polypeptide whose expression is inhibited by the antisense mucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway crequired for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or the product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound; a activity; (11) a culture comprising strains in which the extent or compound.s activity; (11) a culture comprising strains in which the extent or organism. The strains in which the extent or to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the collection of credit discovery programs, or for screening for homologous nucleic acids are useful for crediting proteins or screening for homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, C. required for proliferation in cells other than S. aureus, S. typhimurium, C. prokaryotic sesential genes. Note: The sequence is one of the target or prokaryotic senential genes. Note: The sequence data for this patent did electronic format directly from WIPO at
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Gaps ö 31.6%; Score 83.2; DB 8; Length 1653; 68.0%; Pred. No. 1.5e-17; tive 0; Mismatches 54; Indels 0; Best Local Similarity 68.09 Matches 115; Conservative Query Match

1007 ATACAGGGGAAAAATTGAGATTGCCTTAGACAAGGCTCTGACACCAAATCAAATGCTC 1066 212 93 TGACCACCTATNTGCATCAAGTGCCAAATGACCAGTCGAGTGTGCGGTTAGACAACTACT 152 153 ATACGGGCAAGGAACTGGAGATTGAGTTGGATGTGGCTTTGACTCCTAGCCAAAATGCCC ઠે δ

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Search completed: January 20, 2006, 15:20:15 Job time : 475 secs

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Copyright (c) 1993 - 2006 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES		Description	BY453989 BY453989 BY453989	CB898978 tric016xm	CNS00L12 AL067834 Drosophil	3X368104 BX368104 BX368104	CV072680 Lr_JV2CF_	2A036082 Lr_adE	3M638966 BM638966 170006	BM642048	3M636853 170006875	3M616582 170006871	_	3M628044 170006874	: BM625696 :	3M578413 17000687;	BM618626 1	3M642729 BM642729 170006873	3M627773 170006874	3M649206 170006873	3M648844 170006873	IM632022 170006875	3MG36042 170006875	ONCOCONO ONCOCONO ONCOCONO
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3 BM651776 3 BM625442 3 BM643948 3 BM653819	3 BM656762 3 BM631562 3 BM592722 3 BM591312 5 BM641312	3 BM6270092 10 CG618897 5 BX848199 9 b2108334	6 CA449674 2 BE970931 1 AW553179 2 BG146742	1 AA086663 10 CG887081 2 BB197026 1 AA689925 6 CA322313
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## ALIGNMENTS

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CNSOOL12
Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR22010 of RPCI-98 library from Drosophila melanogaster (fruit [IJy), genomic survey sequence.
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                                                                                                                                                     ricol6xm10 T.reesei mycelial culture, Version 3 april Hypocrea ecorina cDNA clone tricol6xm10, mRNA sequence.
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Foreman, P.K. Brown, D.E., Dankmeyer, L., Dean, R., Diener, S., Dunn-Coleman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S., Dunn-Coleman, N.S., Goedegebuur, F., Houfek, T.D., England, G.J., Kalley, A.S., Meerman, H.J., Mitchhall, r., Mitchinson, C., Olivares, H.A., Teunissen, P.J., Yao, J. and Ward, M.
Transcriptional regulation of biomass-degrading enzymes in the filamentous fungus Trichoderma reesei
J. Biol. Chem. 278 (34), 31988-31997 (2003)
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                                                                                                                                                                                                                                                                                                   Hypocrea jecorina (anamorph: Trichoderma reesei)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         925 Page Mill Road, Palo Alto, CA 94304, USA Tel: (650) 846-7635
Fax: (650) 621-7817
Email: Pforeman@genencor.com
Seq primer: LT-Fl primer.
Location/Qualifiers
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0; Mismatches 116;
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/mol_type="mRNA"
/strain="QM6a"
                                                                                                                                    807 bp
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/clone="tric016xm10"
                                                                                                                                                              tric016xm10 T.reesei mycelial
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              Concactor institute mayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Email: genome-resegescriken.jp, URL:http://genome.gec.riken.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Rukda,S.,
Hirozane,T.: Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nawana,K., Nuramataki,R.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hirozane,T.: Imotani,W., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,T. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Namm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
Genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library Genome Res. 11 (2), 281-289 (2001)
connucter-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Exploration preparatory in Riken
Davision of Experimental Animal Research in Riken contributed to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   255 cccecceseccascrigianiscristriscricassaccesecceisressacce 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="teaxon:1000"
/clone="K630070L23"
/clone=lib=BIKEN full-length enriched, pooled tissues, adult Epleen, etc."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          315 ACGCTATGTGCTCGAAGGCCAGGGCTTGAGTTGTATCTGCGGAAGATCCAAGCCCCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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Best Local Similarity
Matches 74; Conserv
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ORGANISM

AUTHORS JOURNAL

TITLE

COMMENT

RBPERENCE

VERSION KEYWORDS SOURCE

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CV072680 406 bp mRNA linear RST 25-AUG-2004 Lr_JV2CF_27G04 SKplus Juvenile Earthworm Library Lumbricus rubellus CDNA clone Lr_JV2CF_27G04, mRNA sequence.
                                                                                                                                 Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
Lumbricina; Lumbricidae; Lumbricus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Sequencing was performed in Edinburgh using the pBluescript II XR
cDNA library (Stratagene) protocol.
                                                                                                                                                                                                                                                                                                                                                                                        For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOAU013ZD11_U01236_1&c=7464.f. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chaseley,J., Hedley,B.A., Morgan,A.J., Sturzenbaum,S., Kille,P. Blaxter,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195 CTCCTAGCCAAAATGCCCCAGCGGTACTTCAAGAAGTACCAGAAACTCAAGGAGGCGGTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 TGCGGTTAGACAACTACTATACGGGCAAGGAACTGGAGATTGAGTTGGATGTGGCTTTGA
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Tel: +44 2920876680
Fax: +44 2920874305
L.w.B., Gruber,C., Jessee,J. and Polayes,D. Pull-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.1%; Sco. No. 4... 54.3%; Pred. No. 4... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI073YC17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2004)
Contact: Jennifer Chaseley
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                                                                                                               Contact: Genoscope
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                             AUTHORS
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                                                                                                                                                                                                                                                                                                                                                       - Web: www.genoscope.cns.fr.

- Web: www.genoscope.cns.fr.

- Web: www.genoscope.cns.fr.

- Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osocgawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-9 and was constructed by partial BCORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://www.iter.org.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 GTTGGATGTGGCTTTGACTCCTAGCCAAAATGCCCAGCGGGTACTTCAAGAAGTACCAGAA 237
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                            Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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33.2%; Pred. No. 1.7;
tive 47; Mismatches 90;
                                                                                     Drosophila melanogaster (fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="taxon:727"
/clone lib="RPCI-98"
/note="end : TET3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 ACTCAAGGAGGCGGTCAAGCACCTG 262
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                                   GI:4957863
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                                                                                                                                                                                                                            (bases 1 to 1101)
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1 (bases 1 to 850)
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Matches 68; Conservative
                                                                                                                                                                                                                                                                                       Direct Submission
                                   AL067834.1
                                                                                                                                                                                                                                                            Зеповсоре
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Gaps

219

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/db xref="taxon:7165"
/dlone="19600449621565"
/dlone="19600449621565"
/dev stage="Addult"
/lab host="DH10b"
/clone="lib="A.Gam.ad.cDNA1"
/clone="lib="A.Gam.ad.cDNA1"
/note="vector: pSport!; Site=1: Sall; Site=2: Not1; Whole adult mosguitoes (mixed sax) frozen on liquid nitrogen.
cDNA inserts >500 bp cloned directionally into pSport 1.
Not 1 site is 3 . Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       427 bp mRNA linear EST 26-FEB-2002
17000687567125 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
19600449621565 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                        /clone="Lr_adE_01G12"
/tissue_type="whole worm"
/dev_stage="adult"
/clone_llb="Earthworm Lambda Zap Express Library"
/note="Vector: pBK-CMV; The library was prepared using protocol given by supplier (Stratagene)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 CAAGGAACTGGAGATTGAGTTGGATGTGGCTTTGACTCCTAGCCCAAAATGCCCAGCGGTA
                                                                                                                                                                                                                                                              160 CAAGGAACTGGAGATTGAGTTGGATGTGGCTTTGACTCCTAGCCAAAATGCCCAGCGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Culicidae; Anophelinae; Anopheles.
1 (bases 1 to 42?)
Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L.,
Charlab, R., Collins, F.H., Vencer, J.C. and Hoffman, S.L.
Coltar Anopheles gambiae EST project
Unpublished (2002)
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                                                                                                                                                                              Length 648;
                                                                                                                                                                            Score 36.8; DB 5; Length 64
Pred. No. 2.4;
0; Mismatches 27; Indels
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45 w. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
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/mol type="mRNA"
/strain="RSP-ST (Reduced susc.
chromosome)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 2404534580
Email: HoltRA@celera.com
Flate: W01004N8J row: E colt
Seq primer: M13 Reverse.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                    220 CTTCAAGAAGTACCAGAAAC 239
                                                                                                                                                                                                                                                                                                                                                                           335 CATCAAGAAGTTCCAGCAAC 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BM638966.1 GI:18938477
                                                                                                                                                                              14.0%;
                                                                                                                                                                              Query Match
Best Local Similarity 66.2
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59; Conservative
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BM638966
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Sturzenbaum, S., Parkinson, J., Blaxter, M., Morgan, J., Kille, P., Schaffner, W. and Georgiev, O.
Expressed Sequence Tags from the humus earthworm L. rubellus Unpublished (2000)
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Lr adE 01312 T3 Earthworm Lambda Zap Express Library Lumbricus rubellus CDNA clone Lr adE 01312 5' similar to pir|A59287 myosin heavy chain - fluke (Schistosoma mansoni) (strain Brazilian, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Blaxter ML
Institute of Call, Animal and Population Biology
University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 CAAGGAACTGGAGATTGAGTTGGATGTGGCTTTGACTCCTAGCCAAAATGCCCAGCGGTA
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Fax: +44 131 670 5450
Email: mark.blaxter@ed.ac.uk
The library was prepared using protocol given by supplier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                    14.0%; Score 36.8; DB 7; Length 406; 66.2%; Pred. No. 2.1; trive 0; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                              /dev_stage="Juvenile"
/clone_lib="Juvenile_Earthworm_Library"
/note="Organ: Whole_worm"
                                                                                                                                                                        1. .406
/organism="Lumbricus rubellus"
/mol type="mRNA"
/db_xref="taxon:35632"
/clone="Lr_JV2CF_27G04"
PCR PRimers
FORWARD: M13F (gttttcccagtcacgacg)
BACKWARD: M13F (caggaacagctatgaccatg)
Blate: 27 row: G column: 04
Seq primer: Skplus
High quality sequence start: 8
High quality sequence stop: 351.
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Lumbricus rubellus
                                                                                                                                                                                                                                                                                                        tissue_type="Whole worm"
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Seg primer: T3
High quality sequence stop: 457.
Location/Qualifiers
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/db_xref="taxon:35632"
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CA036082.1 GI:24334779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53; Conservative
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PCR PRimers
FORWARD: T3
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Best Local Similarity
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CA036082
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

LOCUS

RESULT 8 BM642048

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db_xxef="texon:7165"
/clone="19600449642127"
/clone="19600449642127"
/de_stage="Adult"
/lab_host="Dhub"
/clone_lib="A.Gam_ad.cDNA1"
/clone_lib="A.Gam_ad.cDNA1"
/clone="Vector: pSport1; Site_1: Sal1; Site_2: Not1; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen.
cDNA inserts >500 bp cloned directionally into pSport 1.
Not 1 site is 3. 'clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."
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17000687148935 A.Gam.ad.cDNA.blood1 Anopheles gambiae cDNA clone
1860049713643 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 CAAGGAACTGGAGATTGAGTTGGATGTGGCTTTGACTCCTAGCCAAAATGCCCAGCGGTA
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea,
Culicidae, Anopheline, Anopheles.
1 (bases 1 to 578)
Holt.R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L.,
Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
Celera Anopheles gambiae EST project
Unpublished (2002)
            Eukaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae; Anophelinae; Anopheles.

1 (bases 1 to 48.4).

Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L. Celera Anopheles gambiae EST project
Unpublished (2002)
Contact: Holt R.A.
Celera Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .486
/organism="Anopheles gambiae"
/mol_type="mRNR"
/strain="RSP-ST (Reduced susc. to Permethrin - std.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38; Indels
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Pred. No. 3.4;
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Fax: 2404533151
Fax: 2404534580
Email: HOlteRa@celera.com
                                                                                                                                                                                                                                                           45 w. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
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                                                                                                                                                                                                                                                                                                                                                                     column: 13
                                                                                                                                                                                                                                                                                                                                        Email: HoltRAgcelera.com
Plate: NUO1003CY2 row: N cc
Seg primer: M13 Reverse.
Location/Qualifiers
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Anopheles gambiae
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17000687562979 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
19600449642127 5', mRNA sequence.
EM636853
                                                                                                                                                                                 476 bp mRNA linear EST 26-FEB-2002
17000687309375 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
19600449651236 5', mRNA sequence.
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//note="Vector: pSport1; Site_1: Sall; Site_2: Not1; Whole adult mosquitcos (mixed sex) frozen on liquid nitrogen.cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mf4.org)."
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Anopheles gambiae
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta; Culicoidea;
Culicidae, Anophelinae, Anopheles.
1 (Bases I to 476)
Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L.,
Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
Celera Anopheles gambiae EST project
Contact: Holt R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to Permethrin - std.
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Best Local Similarity 60.8%; Pred. No. 3.4;
Matches 59; Conservative 0; Mismatches 38; Indels
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                                                                          271 carcadecerraccadeadeagergaadgacerecad 307
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45 w. Gude Dr., Rockville, MD 20850, USA
Tel: 2404534151
Fax: 2404534580
Email: HOLERAGcelera.com
Plate: NU010049W6 row: J column: 02
Seg primer: M13 Reverse.
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/mol rype="mRNA"
/strain="REP-ST (Reduced susc.
chromosome)
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/dev_stage="Adult"
/lab_host="DH10b"
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FEATURES

DEFINITION

BM636853 LOCUS RESULT 9

ACCESSION VERSION KEYWORDS SOURCE

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EST 25-FEB-2002

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219

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EST 26-FEB-2002
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/clone="19600449552861"
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/lab host="DH100"
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/c
cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."
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1 (bases 1 to 607)

Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L. Colera Anopheles gambiae BST project
Contact: Holt R.A.
Celera Genomics

    607
    /organism="Anopheles gambiae"
    /mol_type="mRNA"
    fstrain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"

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17000687497740 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
19600449652861 5', mRNA sequence.
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60.8%; Pred. No. 3.6;
tive 0; Mismatches 38; Indels
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Anopheles gambiae
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Tel: 2404533151
Fax: 2404534580
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13.8%; Score 36.2; DE
Best Local Similarity 60.8%; Pred. No. 3.6;
Matches 59; Conservative 0; Mismatches
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Plate: NU010049VE row: M
Seq primer: M13 Reverse.
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Matches 59; Conserv
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/dev stage="Adult"
/lab_host="DH10b"
/clone lib="A.Gam.ad.cDNA1"
/note="Vector: pSport1; Site_1: Sal1; Site_2: Not1; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen.
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/note="Vector: pSport1; Site 1: Sal1; Site 2: Not1; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen 24 hours after human blood feeding. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Resource Center (www.malaria.mr4.org)"
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Anopheles gambiae
Bukaryota, Metazoa, Arthropoda; Hexapoda, Insecta; Pterygota,
Bukaryota, Metazoa, Arthropoda; Hexapoda, Insecta; Culicoidea;
Culicidae; Anophelinae; Nopheles.
1 (Bases I to 585)
Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L.,
Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
Celera Anopheles gambiae EST project
Contact: Holt R.A.
                                                                                                                                                                                                      to Permethrin - std.
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/strain="RSP-ST (Reduced susc. to Permethrin - std.
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17000687490727 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
18600449669056 5', mRNA sequence.
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Best Local Similarity 60.8%; Pred. No. 3.6;
Matches 59; Conservative 0; Mismatches 38; Indels
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Fax: 2404534580
Fax: 24045346celera.com
Plate: NU01004AYV row: P column: 14
Seq primer: M13 Reverse.
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chromosome)"
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Location/Qualifiers
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BM618626 630 bp mRNA linear EST 25-FEB-2002 17000687439284 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone 19600449662409 5', mRNA sequence.
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/clone lib="A.Gam.ad.cDNA.blood1"
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/clone lib="A.Gam.ad.cDNA.blood1"
/clone lib="A.Gam.ad.cDNA.blood1"
/clone after human blood feeding. cDNA inserts >500 bp cloned directionally into PSport I. Not I site is 3'.
/clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)"
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Anopheles gambiae
Bukaryota, Merazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Culicidae; Anophelinae; Anopheles.
1 (bases 1 to 630)
Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L.,
Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
Celera Anopheles gambiae EST project
Unpublished (2002)
                                      1 (bases 1 to 615)
1 (bases 1 to 615)
2 Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab, R., Collins, P.H., Venter, J.C. and Hoffman, S.L. Celera Anopheles gambiae EST project
Unpublished (2002)
Contact: Holt R.A.
Celera Genomics
45 w. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534800
Email: HoltRA@celera.com
Flate: NU01004AZZ row: D column: 13
Seq primer: M13 Reverse
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Organism="Anopheles gambiae"
/mol type="mRNA"
/strain="RSP-ST (Reduced susc. to Permethrin - std.
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Culicidae; Anophelinae; Anophelea.
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Tel: 2404533151
Fax: 2404534580
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Plate: NU01004185 row: K
Seq primer: M13 Reverse.
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/clone="1960449528977"
/dc ytage="Adult"
/lab_host="PH10b"
/clone=lib="A.Gam.ad.cDNAl"
/nore="Vector: pSport1, Site_1: Sall; Site_2: Not1; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen.
cDNA inserts >500 bp cloned directionally into pSport 1.
Not I site is 3. clones available through the Malaria Research and Reference Reagent Resource Center
(www.malaria.mr4.org)."
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17000687493467 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
8600449628977 5', mRNA sequence.
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Anopheles gambiae
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
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/mol_type="mRNA"
/strain="RSP-ST (Reduced susc. to Permethrin - std.
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      230 CATCAAGGGCTACCAGCAGCAGCTGAAGGACGTCCAG 266
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Fax: 2404534580
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Parai: HOUTRA@Celera.com
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Gaps

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/db xref="taxon:7165"
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/dc gtage="Adult"
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/clone lib="A.Gam.ad.cDNAl"
/clone lib="A.Gam.ad.cDNAl"
/note="Vector: pSportl; Site_1: Sall; Site_2: Notl; Whole adult mosquitces (Mixed sex) frozen on liquid nitrogen.
CDNA inserts >500 bp cloned directionally into pSport 1.
Not 1 site is 3'. Clones available through the Malaxia Research and Reference Reagent Resource Center (www.malaria.mr4.org)."
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Location/Qualifiers
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/organism="Anopheles gambiae"
/nol_type="mRNA"
/fatrain=RSP-ST (Reduced susc. to Permethrin - std.
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